

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Wolf, David L.
Sinha, Uma
- (ii) TITLE OF INVENTION: Agents Affecting Thrombosis and Hemostasis
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Morgan, Lewis & Bockius LLP
 - (B) STREET: 1111 Pennsylvania Avenue, NW
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/671,346
 - (B) FILING DATE: 2000-09-27
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/578,646
 - (B) FILING DATE: 1990-09-04
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/808,329
 - (B) FILING DATE: 1991-12-16
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/249,777
 - (B) FILING DATE: 1994-05-26
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/268,003
 - (B) FILING DATE: 1994-06-29
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/469,301
 - (B) FILING DATE: 1995-06-06
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/016,403
 - (B) FILING DATE: 1998-01-30
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/362,207
 - (B) FILING DATE: 1999-07-28

- (viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 488 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: both

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: -17
 (D) OTHER INFORMATION: /note= "Location of Intron A"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: (37^38)
 (D) OTHER INFORMATION: /note= "Location of Intron B"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 46
 (D) OTHER INFORMATION: /note= "Location of Intron C"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 63
 (D) OTHER INFORMATION: /note= "Xaa = beta-hydroxy aspartic acid."

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 84
 (D) OTHER INFORMATION: /note= "Location of Intron D"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 128
 (D) OTHER INFORMATION: /note= "Location of Intron E"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: (209^210)
 (D) OTHER INFORMATION: /note= "Location of Intron F"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 249
 (D) OTHER INFORMATION: /note= "Location of Intron G"

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: -40..0
 (D) OTHER INFORMATION: /note= "Pre-Pro leader sequence"

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..139
 (D) OTHER INFORMATION: /note= "Factor Xa- Light chain"

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 143..194
 (D) OTHER INFORMATION: /note= "Activation Peptide"

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 195..448
 (D) OTHER INFORMATION: /note= "Factor Xa-Heavy Chain"

(ix) FEATURE:
 (A) NAME/KEY: Disulfide-bond
 (B) LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
 ..109, 111..124, 132..302, 201..206, 221..237,
 350..364, 375..403)

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 39
 (D) OTHER INFORMATION: /note= "Xaa = gamma-carboxy glutamic
 acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Gly	Arg	Pro	Leu	His	Leu	Val	Leu	Leu	Ser	Ala	Ser	Leu	Ala	Gly
-40					-35					-30					-25
Leu	Leu	Leu	Leu	Gly	Glu	Ser	Leu	Phe	Ile	Arg	Arg	Glu	Gln	Ala	Asn
			-20						-15						-10
Asn	Ile	Leu	Ala	Arg	Val	Thr	Arg	Ala	Asn	Ser	Phe	Leu	Xaa	Xaa	Met
	-5							1				5			
Lys	Lys	Gly	His	Leu	Xaa	Arg	Xaa	Cys	Met	Xaa	Xaa	Thr	Cys	Ser	Tyr
	10					15						20			
Xaa	Xaa	Ala	Arg	Xaa	Val	Phe	Xaa	Asp	Ser	Asp	Lys	Thr	Asn	Xaa	Phe
25					30					35					40

Trp Asn Lys Tyr Lys Asp Gly Asp Gln Cys Glu Thr Ser Pro Cys Gln
 45 50 55
 Asn Gln Gly Lys Cys Lys Xaa Gly Leu Gly Glu Tyr Thr Cys Thr Cys
 60 65 70
 Leu Glu Gly Phe Glu Gly Lys Asn Cys Glu Leu Phe Thr Arg Lys Leu
 75 80 85
 Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln Phe Cys His Glu Glu Gln
 90 95 100
 Asn Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn
 105 110 115 120
 Gly Lys Ala Cys Ile Pro Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr
 125 130 135
 Leu Glu Arg Arg Lys Arg Ser Val Ala Gln Ala Thr Ser Ser Ser Gly
 140 145 150
 Glu Ala Pro Asp Ser Ile Thr Trp Lys Pro Tyr Asp Ala Ala Asp Leu
 155 160 165
 Asp Pro Thr Glu Asn Pro Phe Asp Leu Leu Asp Phe Asn Gln Thr Gln
 170 175 180
 Pro Glu Arg Gly Asp Asn Asn Leu Thr Arg Ile Val Gly Gly Gln Glu
 185 190 195 200
 Cys Lys Asp Gly Glu Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu
 205 210 215
 Asn Glu Gly Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile Leu
 220 225 230
 Thr Ala Ala His Cys Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val
 235 240 245
 Gly Asp Arg Asn Thr Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu
 250 255 260
 Val Glu Val Val Ile Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp
 265 270 275 280
 Phe Asp Ile Ala Val Leu Arg Leu Lys Thr Pro Ile Thr Phe Arg Met
 285 290 295
 Asn Val Ala Pro Ala Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr
 300 305 310
 Leu Met Thr Gln Lys Thr Gly Ile Val Ser Gly Phe Gly Arg Thr His
 315 320 325
 Glu Lys Gly Arg Gln Ser Thr Arg Leu Lys Met Leu Glu Val Pro Tyr
 330 335 340

Val Asp Arg Asn Ser Cys Lys Leu Ser Ser Ser Phe Ile Ile Thr Gln
 345 350 355 360
 Asn Met Phe Cys Ala Gly Tyr Asp Thr Lys Gln Glu Asp Ala Cys Gln
 365 370 375
 Gly Asp Ser Gly Gly Pro His Val Thr Arg Phe Lys Asp Thr Tyr Phe
 380 385 390
 Val Thr Gly Ile Val Ser Trp Gly Glu Gly Cys Ala Arg Lys Gly Lys
 395 400 405
 Tyr Gly Ile Tyr Thr Lys Val Thr Ala Phe Leu Lys Trp Ile Asp Arg
 410 415 420
 Ser Met Lys Thr Arg Gly Leu Pro Lys Ala Lys Ser His Ala Pro Glu
 425 430 435 440
 Val Ile Thr Ser Ser Pro Leu Lys
 445

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: both

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: /note= "Factor Xa-Light Chain"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -40..0
- (D) OTHER INFORMATION: /note= "Pre-Pro leader sequence"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: -17
- (D) OTHER INFORMATION: /note= "Location of Intron A"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: (37^38)
- (D) OTHER INFORMATION: /note= "Location of Intron B"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 46
- (D) OTHER INFORMATION: /note= "Location of Intron C"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 63
 (D) OTHER INFORMATION: /note= "Xaa = beta-hydroxy aspartic acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 84
 (D) OTHER INFORMATION: /note= "Location of Intron D"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 128
 (D) OTHER INFORMATION: /note= "Location of Intron E"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: (158^159)
 (D) OTHER INFORMATION: /note= "Location of Intron F"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 198
 (D) OTHER INFORMATION: /note= "Location of Intron G"

(ix) FEATURE:
 (A) NAME/KEY: Disulfide-bond
 (B) LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
 ..109, 111..124, 132..251, 150..155, 170..186,
 299..313, 324..352)

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 39
 (D) OTHER INFORMATION: /note= "Xaa = gamma-carboxy glutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Arg	Pro	Leu	His	Leu	Val	Leu	Leu	Ser	Ala	Ser	Leu	Ala	Gly
-40						-35				-30					-25
Leu	Leu	Leu	Leu	Gly	Glu	Ser	Leu	Phe	Ile	Arg	Arg	Glu	Gln	Ala	Asn
				-20					-15						-10
Asn	Ile	Leu	Ala	Arg	Val	Thr	Arg	Ala	Asn	Ser	Phe	Leu	Xaa	Xaa	Met
		-5						1				5			
Lys	Lys	Gly	His	Leu	Xaa	Arg	Xaa	Cys	Met	Xaa	Xaa	Thr	Cys	Ser	Tyr
10					15						20				
Xaa	Xaa	Ala	Arg	Xaa	Val	Phe	Xaa	Asp	Ser	Asp	Lys	Thr	Asn	Xaa	Phe
25					30					35					40
Trp	Asn	Lys	Tyr	Lys	Asp	Gly	Asp	Gln	Cys	Glu	Thr	Ser	Pro	Cys	Gln

45	50	55
Asn Gln Gly Lys Cys Lys Xaa Gly Leu Gly Glu Tyr Thr Cys Thr Cys		
60	65	70
Leu Glu Gly Phe Glu Gly Lys Asn Cys Glu Leu Phe Thr Arg Lys Leu		
75	80	85
Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln Phe Cys His Glu Glu Gln		
90	95	100
Asn Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn		
105	110	115
Gly Lys Ala Cys Ile Pro Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr		
125	130	135
Leu Glu Arg Arg Lys Arg Arg Ile Val Gly Gly Gln Glu Cys Lys Asp		
140	145	150
Gly Glu Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu Asn Glu Gly		
155	160	165
Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile Leu Thr Ala Ala		
170	175	180
His Cys Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val Gly Asp Arg		
185	190	195
Asn Thr Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu Val Glu Val		
205	210	215
Val Ile Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp Phe Asp Ile		
220	225	230
Ala Val Leu Arg Leu Lys Thr Pro Ile Thr Phe Arg Met Asn Val Ala		
235	240	245
Pro Ala Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr Leu Met Thr		
250	255	260
Gln Lys Thr Gly Ile Val Ser Gly Phe Gly Arg Thr His Glu Lys Gly		
265	270	275
Arg Gln Ser Thr Arg Leu Lys Met Leu Glu Val Pro Tyr Val Asp Arg		
285	290	295
Asn Ser Cys Lys Leu Ser Ser Ser Phe Ile Ile Thr Gln Asn Met Phe		
300	305	310
Cys Ala Gly Tyr Asp Thr Lys Gln Glu Asp Ala Cys Gln Gly Asp Ser		
315	320	325
Gly Gly Pro His Val Thr Arg Phe Lys Asp Thr Tyr Phe Val Thr Gly		
330	335	340
Ile Val Ser Trp Gly Glu Gly Cys Ala Arg Lys Gly Lys Tyr Gly Ile		

345	350	355	360
Tyr Thr Lys Val Thr Ala Phe Leu Lys Trp Ile Asp Arg Ser Met Lys			
	365	370	375
Thr Arg Gly Leu Pro Lys Ala Lys Ser His Ala Pro Glu Val Ile Thr			
	380	385	390
Ser Ser Pro Leu Lys			
	395		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: both

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: -40..397
- (D) OTHER INFORMATION: /note= "Same features apply from

SEQ ID NO:2"

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: /note= "Factor Xa - Light Chain"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -40..0
- (D) OTHER INFORMATION: /note= "Pre-Pro leader sequence"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: -17
- (D) OTHER INFORMATION: /note= "Location of Intron A"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: (37^38)
- (D) OTHER INFORMATION: /note= "Location of Intron B"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 46
- (D) OTHER INFORMATION: /note= "Location of Intron C"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 63
- (D) OTHER INFORMATION: /note= "Xaa= beta-hydroxy aspartic acid."

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 84
 (D) OTHER INFORMATION: /note= "Location of Intron D"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: (158^159)
 (D) OTHER INFORMATION: /note= "Location of Intron F"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 198
 (D) OTHER INFORMATION: /note= "Location of Intron G"
- (ix) FEATURE:
 (A) NAME/KEY: Disulfide-bond
 (B) LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96
 ..109, 111..124, 132..251, 150..155, 170..186,
 299..313, 324..352)
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 39
 (D) OTHER INFORMATION: /note= "Xaa = gamma-carboxy glutamic
 acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Gly	Arg	Pro	Leu	His	Leu	Val	Leu	Leu	Ser	Ala	Ser	Leu	Ala	Gly	-40	-35	-30	-25
Leu	Leu	Leu	Leu	Gly	Glu	Ser	Leu	Phe	Ile	Arg	Arg	Glu	Gln	Ala	Asn	-20	-15	-10	
Asn	Ile	Leu	Ala	Arg	Val	Thr	Arg	Ala	Asn	Ser	Phe	Leu	Xaa	Xaa	Met	-5	1	5	
Lys	Lys	Gly	His	Leu	Xaa	Arg	Xaa	Cys	Met	Xaa	Xaa	Thr	Cys	Ser	Tyr	10	15	20	
Xaa	Xaa	Ala	Arg	Xaa	Val	Phe	Xaa	Asp	Ser	Asp	Lys	Thr	Asn	Xaa	Phe	25	30	35	40
Trp	Asn	Lys	Tyr	Lys	Asp	Gly	Asp	Gln	Cys	Glu	Thr	Ser	Pro	Cys	Gln	45	50	55	
Asn	Gln	Gly	Lys	Cys	Lys	Xaa	Gly	Leu	Gly	Glu	Tyr	Thr	Cys	Thr	Cys	60	65	70	
Leu	Glu	Gly	Phe	Glu	Gly	Lys	Asn	Cys	Glu	Leu	Phe	Thr	Arg	Lys	Leu	75	80	85	
Cys	Ser	Leu	Asp	Asn	Gly	Asp	Cys	Asp	Gln	Phe	Cys	His	Glu	Glu	Gln				

90	95	100
Asn Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn 105 110 115 120		
Gly Lys Ala Cys Ile Pro Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr 125 130 135		
Leu Glu Arg Arg Lys Arg Arg Ile Val Gly Gly Gln Glu Cys Lys Asp 140 145 150		
Gly Glu Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu Asn Glu Gly 155 160 165		
Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile Leu Thr Ala Ala 170 175 180		
His Cys Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val Gly Asp Arg 185 190 195 200		
Asn Thr Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu Val Glu Val 205 210 215		
Val Ile Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp Phe Asn Ile 220 225 230		
Ala Val Leu Arg Leu Lys Thr Pro Ile Thr Phe Arg Met Asn Val Ala 235 240 245		
Pro Ala Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr Leu Met Thr 250 255 260		
Gln Lys Thr Gly Ile Val Ser Gly Phe Gly Arg Thr His Glu Lys Gly 265 270 275 280		
Arg Gln Ser Thr Arg Leu Lys Met Leu Glu Val Pro Tyr Val Asp Arg 285 290 295		
Asn Ser Cys Lys Leu Ser Ser Ser Phe Ile Ile Thr Gln Asn Met Phe 300 305 310		
Cys Ala Gly Tyr Asp Thr Lys Gln Glu Asp Ala Cys Gln Gly Asp Ala 315 320 325		
Gly Gly Pro His Val Thr Arg Phe Lys Asp Thr Tyr Phe Val Thr Gly 330 335 340		
Ile Val Ser Trp Gly Glu Gly Cys Ala Arg Lys Gly Lys Tyr Gly Ile 345 350 355 360		
Tyr Thr Lys Val Thr Ala Phe Leu Lys Trp Ile Asp Arg Ser Met Lys 365 370 375		
Thr Arg Gly Leu Pro Lys Ala Lys Ser His Ala Pro Glu Val Ile Thr 380 385 390		
Ser Ser Pro Leu Lys		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

GTCGACTCTA GAGGGGCTGG CAGGAATTCC GCATGGGGCG CCCACTGCAC CTCGTCCTGC      60
TGAGTGCCTG CCTGGCTGGC CTCCTGCTGC TCGGGGAAAG TCTGTTCATC CGCAGGGAGC      120
AGGCCAACAA CATCCTGGCG AGGGTCACGA GGGCCAATTC CTTTCTTGAA GAGATGAAGA      180
AAGGACACCT CGAAAGAGAG TGCATGGAAG AGACCTGCTC ATACGAAGAG GCCCGCGAGG      240
TCTTTGAGGA CAGCGACAAG ACGAATGAAT TCTGGAATAA ATACAAAGAT GGCGACCACT      300
GTGAGACCAG TCCTTGCCAG AACCAGGGCA AATGTAAAGA CGGCCTCGGG GAATACACCT      360
GCACCTGTTT AGAAGGATTC GAAGGCAAAA ACTGTGAATT ATTCACACGG AAGCTCTGCA      420
GCCTGGACAA CGGGGACTGT GACCAGTTCT GCCACGAGGA ACAGAACTCT GTGGTGTGCT      480
CCTGCGCCCG CGGGTACACC CTGGCTGACA ACGGCAAGGC CTGCATTCCC ACAGGGCCCT      540
ACCCCTGTGG GAAACAGACC CTGGAACGCA GGAAGAGGTC AGTGGCCCAG GCCACCAGCA      600
GCAGCGGGGA GGCCCCTGAC AGCATCACAT GGAAGCCATA TGATGCAGCC GACCTGGACC      660
CCACCGAGAA CCCCTTCGAC CTGCTTGACT TCAACCAGAC GCAGCCTGAG AGGGGCGACA      720
ACAACCTCAC CAGGATCGTG GGAGGCCAGG AATGCAAGGA CGGGGAGTGT CCCTGGCAGG      780
CCCTGCTCAT CAATGAGGAA AACGAGGGTT TCTGTGGTGG AACTATTCTG AGCGAGTTCT      840
ACATCCTAAC GGCAGCCCAC TGTCTCTACC AAGCCAAGAG ATTCAAGGTG AGGTAAGGGG      900
ACCGGAACAC GGAGCAGGAG GAGGGCGGTG AGGCGGTGCA CGAGGTGGAG GTGGTCATCA      960
AGCACAACCG GTTCACAAAG GAGACCTATG ACTTCGAGAT CGCCGTGCTC CGGCTCAAGA     1020
CCCCCATCAC CTTCCGCATG AACGTGGCGC CTGCCTGCCT CCCCAGAGCGT GACTGGGCCG     1080
AGTCCACGCT GATGACGCAG AAGACGGGGA TTGTGAGCGG CTTGCGGCGC ACCCACGAGA     1140
AGGGCCGGCA GTCCACCAGG CTCAAGATGC TGGAGGTGCC CTACGTGGAC CGCAACAGCT     1200
GCAAGCTGTC CAGCAGCTTC ATCATCACCC AGAACATGTT CTGTGCCGGC CGTCACCCGC     1260

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TTCAAGGACA CCTACTTCGT GACAGGCATC GTCAGCTGGG GAGAGGGCTG TGCCCGTAAG	1320
GGGAAGTACG GGATCTACAC CAAGGTCACC GCCTTCCTCA AGTGGATCGA CAGGTCCATG	1380
AAAACCAGGG GCTTGCCCAA GGCCAAGAGC CATGCCCCGG AGGTCATAAC GTCCTCTCCA	1440
TTAAAGTGAG CGTCCTCTCC ATCCCACTCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1500

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg	Lys	Arg	Arg	Lys	Arg
1				5	

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCCGAGGGG ACGCCGGGGG CCCGCAC	27
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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACCTATGACT TCAACATCGC CGTGCTC

27

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACCCTGGAAC GCAGGAAGAG GATCGTGGGA GGCCAGGAAT GC

42

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACCCTGGAAC GCAGGAAGAG GAGAATCGTG GGAGGCCAGG AATGC

45

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACCCTGGAAC GCAGGAAGAG GCGGAAAAGA ATCGTGGGAG GCCAGGAATG C

51

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACCCTGGAAC GCAGGAAGAG GCCTAGGCCA TCTCGGAAAC GCAGGATCGT GGGAGGCCAG 60

GAATGC 66